



Analysis of genetic divergence through agronomic characters in green corn cultivars

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Abstract— The genetic divergence in maize populations is important, as it allows us to identify among the existing genotypes, the best ones to be used as parents in future breeding programs as a strategy for obtaining greater gains. Therefore, the objective of this work was to estimate the genetic divergences in green corn cultivars. The tests were conducted in the 2019/20 harvest on a property in the state of Pará. The design used in the given experiment was randomized blocks (DBC) and 3 replicates. The experimental plot consisted of 4 rows of 5.0 m spaced at 0.9 m between rows, the two central rows being considered the useful area. The genetic divergence was evaluated by multivariate procedures such as the generalized Mahalanobis distance and by Tocher optimization grouping methods and Singh criterion to quantify the relative contribution of the seven characteristics. The characteristics average mass of grains per ear and number of grains in the row of the ear were the ones that most contributed to genetic divergence. The dual hybrids BR205 and BRS3046 and the triple hybrid AG8088 are potentially promising for use in future breeding programs.

I. INTRODUCTION

In Brazil, the amount of total maize produced in 2020/2021 can come to 108,068 thousand tons of corn in the country, with emphasis on the volume predicted in the second harvest, which represents almost 77% of this total. With an increase in 5.4% in relation to the harvest 2019/20. The total planted area was stimulated in 19,495.2 thousand hectares, with a productivity of 5543 kg ha⁻¹ [1].

In Brazil, around 36 thousand hectares of sweet corn, and practically 100% production are intended for industrial processing for human consumption, with movement around R\$ 550 million a year, which is why it is also

called special corn. This follow-up has grown in recent years and the trend is the maintenance of this growth, aiming at the internal and foreign market. One of the factors that did not allow the consumption of sweet corn to be spread more rapidly among Brazilians was the lack of cultivars adapted to our environment conditions, in its almost full tropical [2].

The sweet corn harvest is carried out when the grains are still high in moisture (greater than 70%), which highlights the interference of the physiological stage of grain maturity in the yield. Therefore, the most propitious time for harvesting is the period in which the grains reach

the maximum point of dry matter accumulation and water content. This interval, known as the useful harvest period, varies between genotypes [3].

Due to the need for cultivars that present specific characteristics for the green corn market, private companies and public research institutions have intensified in breeding programs artificial selection schemes aimed at obtaining genotypes that meet the minimum requirements of the consumer market. In the selection, it should be taken into account the obtaining of genotypes with high yield potential, pericarp texture, adaptability and productive stability, which will allow its wide recommendation for cultivation [4]. However, even with the advance of genetic improvement, the availability of cultivars recommended for green corn production is scarce, and often farmers end up using specific genotypes for grain production or silage, which generates disinformation of the product, which end up not meeting the minimum requirements of the consumer market.

The study of genetic diversity through multivariate analysis is important for breeding programs, as the variability among genotypes is essential to obtain selection gains in crosses of genetically divergent groups that present characteristics of interest [5].

Genetic divergence has been studied in several cultures based on morphoagronomic, molecular and both characters, aiming at the selection of parents for the formation of hybrid combinations and/or formation of new segregating populations from crosses with more divergent genotypes [5].

The more divergent the parents, the greater the resulting variability in the segregating population, and the more likely it is to regroup allows into new favorable combinations [6]. Among the various dissimilarity measures proposed for the quantification of distances between genotypes, the generalized distance of Mahalanobis has been the most widely used when experimenting with repetitions [7]. This differs from other techniques by taking into account the correlations between the characters evaluated [5].

There are several studies of genetic divergence involving the culture of acai [8], cotton [9], carrot [10], broad bean [11], bean [12 and 13], passion fruit [14], melon [15], corn [16 and 17] and wheat [18]. Than has been guiding the bestists in the proper choice of parents.

With the advent of new technologies and studies, these techniques have become more common among specialist and corn crop improver [7, 8, 19, 20, 21, 22, 23, 24, 25 and 26].

Based on this model, the main objective of the study was to estimate genetic divergence through agronomic characters in 12 green corn cultivars in the crop 19/20 in the municipality of Santa Maria of Barreiras, State of Pará.

II. MATERIAL AND METHODS

The experiment was carried out at Sítio Vitória, located in the municipality of Santa Maria of Barreiras -PA, in sowing carried out on November 28, 2019, in the transition from the cerrado biome to the Amazon biome (Figure 1).

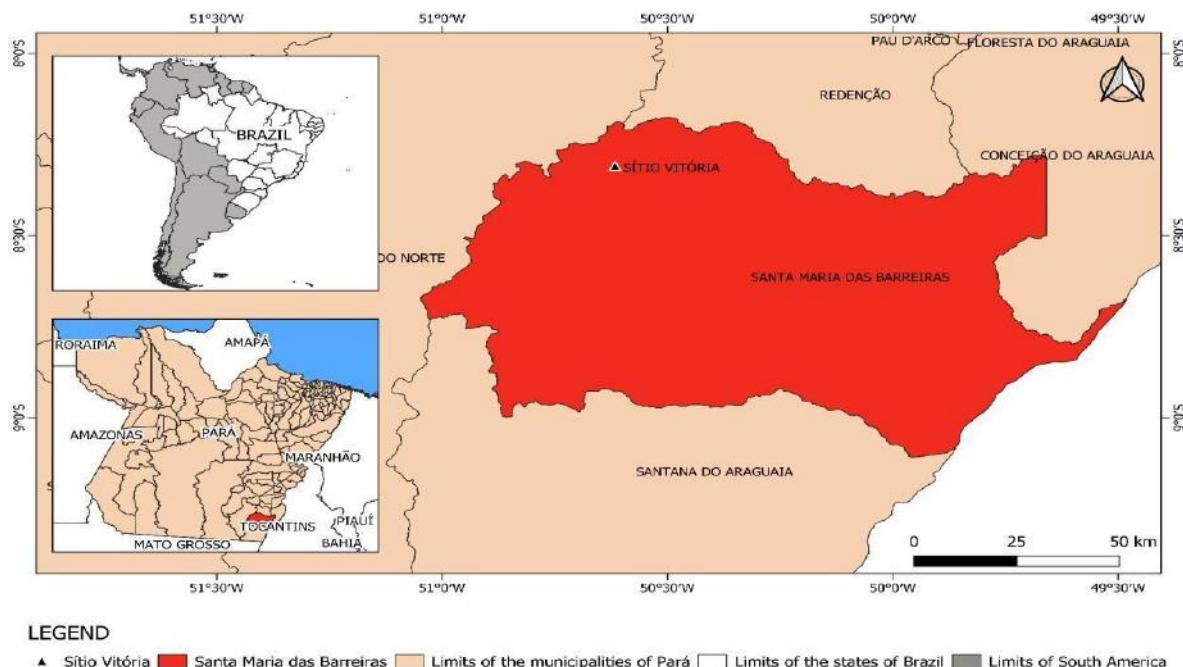


Fig.1. Location Map of Sítio Vitória, in the municipality of Santa Maria of Barreiras, State of Pará.

The region has a predominantly tropical climate according to Koppen the Aw, with rains in summer and with a distinctly dry season in winter, and the precipitation

and temperature data obtained over the conduction period of the experiment are shown in Figure 2.

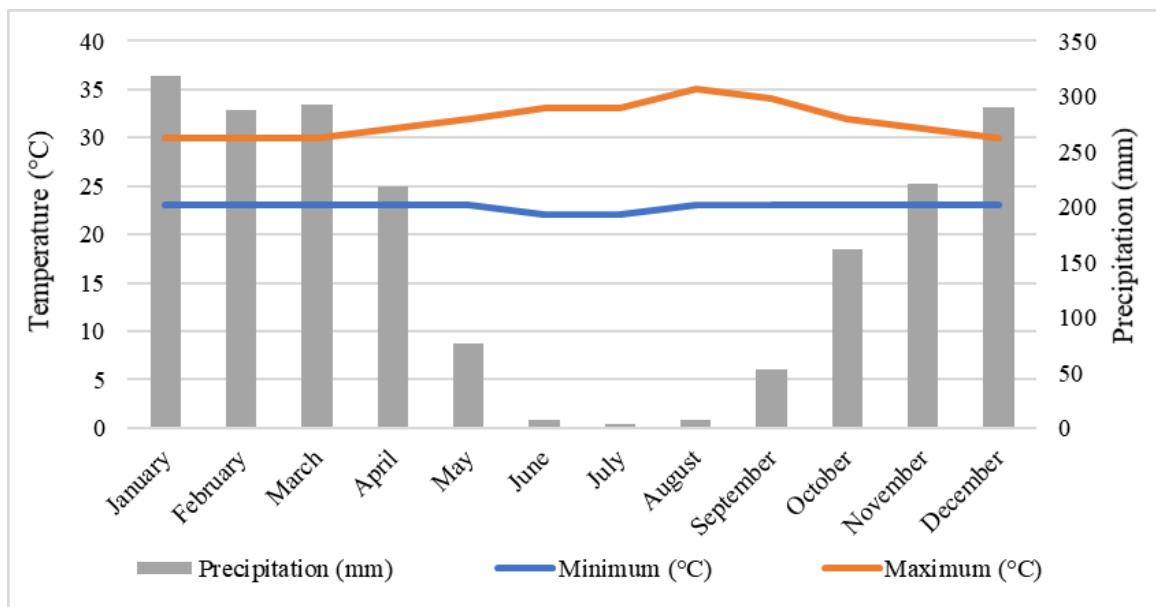


Fig. 2: Precipitation climatological averages, minimum temperature and maximum of the municipality of Santa Maria of Barreiras, Estado of the Pará in the year of 2019.

Fonte: Climatempo [20].

The results of the chemical analysis and soil texture are presented in Table 1.

Table 1. Chemical attributes and soil granulometry used in the first epoch of the experiment. Santa Maria of Barreiras-Pará, 2018.

pH	P meh	K	S	Ca ⁺²	Mg ⁺²	Al ⁺³	H+Al	M.O.	C.O.
CaCl ₂	mg.dm ⁻³				cmolc.dm ⁻³			dag.kg ⁻¹	%
4.8	4.9	43	3.0	1.7	0.3	0.20	3.10	1.7	1.0
SB	CTCt		V %		m	Clay	silt	sand full	
			mg.dm ⁻³					%	
2.11	5.21		40		9.0	15.0	5.0		80.0

Font: Solocria [28].

The experimental design used was randomized blocks (DBC) with 12 treatments and three replications. The treatments consisted of maize cultivars, three pollination varieties, open, one single hybrid, seven double hybrids

and a triple hybrid, whose characteristics are found in Table 2. The experimental plot consisted of 4 rows spaced from 5.0 m in length per 0.9 m between rows, and the two central rows were considered as a useful area.

Table 2. Agronomic characteristics of corn cultivars used in the experiment.

Name	Base	Transgenics	Cycle	Finality	Level
AG 1051	HD	C	SMP	G/MV/SPI	M/A
AG 8088 PRO2	HS	PRO2	P	G/SPI	A
ALBANDEIRANTE	PPA	C	SMP	G/SPI	B/M

ANHEMBI	PPA	C	P	G/SPI	B/M
BM 3051	HD	C	P	MV/SPI	M/A
BR 2022	HD	C	P	G/SPI	M/A
BR 205	HD	C	P	G/SPI	M/A
BR 206	HD	C	P	G/SPI	M/A
BRS 3046	HT	C	SMP	MV	M/A
CATIVERDE	PPA	C	SMP	MV/SPI	M
M 274	HD	C	P	G/SPI	B/M
PR 27D28	HD	C	SP	G/SPI	B/M

HS: Simple hybrid; HD: Double hybrid; HT: Triple hybrid; PRO2: technology VT PRO 2™; C: conventional; P: precocious; SMP: Semi-early; SP: Superprecococe; G: grain; MV: Green corn; SPI: Silage of whole plant; A: high; M: Medium B: low.

Soil tillage was performed in the conventional system, with a gradation followed by leveling the field. Pre-planting fertilization was calculated according to nutritional levels obtained through soil analysis (Table 1), being applied manually using 300 kg ha⁻¹ of the formulated 5-25-15 (N-P₂O₅-K₂O) + 0,5% Zn. Where urea was used (45% from N) as the source of N, resulting in the full of 266 kg ha⁻¹, that have been fragmented into two applications, in the phenological V4 and V8, according to Ribeiro et al. [29].

The sowing was performed manually in the groove with an approximate depth of 0.04 m, immediately after seedling emergence, thinning was carried out to obtain the spacingde 0.02 m between plants, with the aim of obtaining a final population of 55,555 plants/ha.

Cultural treatments, such as phytosanitary control of diseases, pests and weeds were carried out according to the technical recommendations of the crop [30].

The harvest was carried out in the R3, in the two central rows, as it is when it is best suited for fresh consumption or processed [30].

The following characteristics were analyzed: plant height (AP) (cm), spike height (AE) (cm), ear weight with straw (PECP) (g), weight of the ear without straw (PESP) (g), spike length (CE) (mm), ear diameter (DE) (mm),

number of grains per row (NGE) and average grain mass per ear (MGE) (g). The descriptors were measured according to the Embrapa [2].

For the analysis of genetic divergence, measures of dissimilarities were used that were determined according to the multivariate analysis model, thus allowing the obtaining of dissimilarities, residual covariances and means of populations.

To establish similes groups, the grouping method was applied by optimization of Tocher [31], calculations of which were based on the generalised distance of Mahalanobis (D^2) [32], and the criterion of Singh [33] to quantify the relative contribution of the seven traits evaluated in genetic divergence.

Statistical analyses were performed using the Computational Genes program, 2007 [34].

III. RESULTS AND DISCUSSION

Measures of genetic dissimilarity, estimated from the distance of Mahalanobis (Table 3), presented a high magnitude (9.72 the 70.70), indicating the presence of genetic variability among genotypes. Sodré et al. [26] found the magnitude of D^2 from 0.4 the 328.7 and Santos et al. [22] found magnitude ($D^2 = 4.0$ the 644.6) corn crop.

Table 3. Estimation of distances from Mahalanobis (D^2) maximum and minimum number of maize genotypes.

Cultivate	Distance D^2 among genotypes		
	Bigger	Cultivate	Minor
ANHEMBI	45.23	(BR205)	11.71
BR2022	28.34	(BR205)	9.72

CATIVERDE	62.57	(BRS3046)	14.29	(BR205)
M274	43.57	(BR205)	10.27	(ALBANDEIRANTE)
AG 1051	69.78	(BR205)	11.74	(BM3051)
AG8088	51.39	(AG 1051)	13.17	(BR2022)
PR27D28	43.68	(BRS3046)	13.55	(BR206)
BR205	70.70	(BRS3046)	14.29	(CATIVERDE)
BRS3046	70.70	(BR205)	20.57	(BM3051)
BM3051	61.93	(BR205)	11.74	(AG 1051)
ALBANDEIRANTE	38.92	(BR205)	9.93	(BR2022)
BR206	28.00	(M274)	9.72	(BR2022)
Longer distance		70.70		(BR205 x BRS3046)
Shorter distance		9.72		(BR2022 x BR206)

In parentheses are represents cultivar(s).

The combination of cultivars BR205 x BRS3046 (Table 3) were considered the most divergent ($D^2 = 70.7$), followed by AG 1051 x BR205 ($D^2 = 69.78$). The shortest distances were between the combinations BR2022 x BR206, AL BANDEIRANTE x BR2022 and M274 x ALBANDEIRANTE ($D^2 = 9.72; 9.93; 10.27$ respectively). Combinations that result in longer distances represent genotypes that come from distinct germplasm banks, and shorter distances, materials that are probably from the same germplasm bank [22, 23, 25 and 35].

According to Santos et al. [7], the analysis of the genetic distance between cultivars leads to a faster, lower use of labor and financial resources that will be used in future programs to improve corn, because it allows the evaluation of distinct and promising materials to be inserted in breeding programs.

Table 4. Grouping by the Tocher method, based on the dissimilarity expressed by the generalized Mahalanobis distance.

Group	Access
I	BR2022, BR206, ANHEMBI, ALBANDEIRANTE, CATIVERDE and PR27D28
II	AG 1051, BM3051 and M274
III	AG8088 and BR205
IV	BRS3046

The first large group separated by the Tocher was composed of six cultivars (BR2022, BR206, ANHEMBI, ALBANDEIRANTE, CATIVERDE and PR27D28), the second by three (AG 1051, BM3051 and M274), the third group was formed by two cultivars (AG8088 and BR 205) and the room by the single cultivate (BRS3046).

To achieve, the desired maximum level of heterosis is necessary to make combinations between materials that are complementary, that is, in the locus where there are recessive alllinks in one material, in the other the allele must be dominant and vice versa, thus generating the greater degree of heterosis [22].

Cluster analysis by Tocher method separates materials into distinct groups, so that there is intragroup homogeneity and intergroup heterogeneity [5]. After the dissimilarity measurements (D^2) were obtained, the cultivars were grouped into four groups (Table 4).

Groups formed by few genotypes indicate that they are divergent in relation to the others, facilitating the prospection of work in breeding programs [22, 23, 25 and 35].

The mean intergroup distances from the method of optimising Tocher (Table 5), indicate which groups are the most divergent. Thus, the least divergent groups were I

and II (23.96); and II and IV (27.17) (Table 5) and the most divergent were III and IV (56.43); and II and III (48.88).

Divergent groups can be used the basis for developing strains that will serve the future hybrid crosses, they require additional loci [16].

Table 5. Average distances between groups formed by genetic divergence analysis in maize genotypes.

Group	II	III	IV
I	23.96	27.97	35.46
II		48.88	27.17
III			56.43

Regarding the contribution of the characteristics to the study of genetic divergence (Table 6), the one that most contributed was the MGE (25.59%), followed by the number of grains per row (NGF) (17.63%). The lowest contributions were of the characteristics PECP (5.66%)

In this sense, the double hybrids BR205 and BRS3046 and the triple hybrid AG8088, because they are the most divergent (Table 3), are in distinct clusters (Table 4) and with the greater intergroup distance (Table 5), are potentially promising for use in future breeding programs in hybridization or self-fertilization processes for the extraction of strains.

Table 6. Relative contribution of traits in the genetic dissimilarity of genotypes.

Variable	Value in%
Plant height (AP)	12.96
Spike height (AE)	12.39
Ear weight with straw (PECP)	5.66
Ear weight without straw (PESP)	6.16
Number of grains per row (NGF)	17.63
Ear length (CE)	9.63
Ear diameter (DE)	9.98
Average grain mass per ear (MGE)	25.59

IV. CONCLUSION

The characteristics of average grain mass per ear and number of grains in the ear row were the ones that most contributed to genetic divergence.

Hybrids BR205 and BRS3046 and the hybrid BR205 and AG1051 are potentially promising for use in future breeding programs.

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